

<110> Karolinska Innovations AB  
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Karlgren, Maria  
Gomez, Alvin

<120> Drug target in cancer therapy

<130> P05980PC00/HAM/em

<150> SE0203137-5

<151> 2002-10-24

<150> US 60/420,787

<151> 2002-10-24

<160> 10

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Homo sapiens

<220>

<221> Primer

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27

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## sequence\_listing.ST25.txt

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<213> Homo sapiens

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<211> 23

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<210> 4

<211> 23

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<213> homo sapiens

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<222> (1)..(23)

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## sequence\_listing.ST25.txt

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<211> 28

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<222> (1)..(28)

## sequence\_listing.ST25.txt

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28

&lt;210&gt; 8

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 8

Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu Leu Gly Leu Trp Gly  
1 5 10 15Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro Ala Ala Arg Trp Pro  
20 25 30Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg  
35 40 45Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly  
50 55 60Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr  
65 70 75 80Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu  
85 90 95Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly  
100 105 110Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe  
115 120 125Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala  
130 135 140Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly  
145 150 155 160Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser  
165 170 175Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp  
180 185 190

## sequence\_listing.ST25.txt

Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu  
 195 200 205

Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly  
 210 215 220

Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val  
 225 230 235 240

Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys  
 245 250 255

Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly  
 260 265 270

Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala  
 275 280 285

Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr  
 290 295 300

Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly  
 305 310 315 320

Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro  
 325 330 335

Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His  
 340 345 350

Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr  
 355 360 365

Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro  
 370 375 380

Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln  
 385 390 395 400

Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His  
 405 410 415

Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val  
 420 425 430

Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala  
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Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro  
 450 455 460

## sequence\_listing.ST25.txt

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Ala Gln Ala Leu Cys Ala Val Pro Arg Pro  
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<211> 2432

<212> DNA

<213> homo sapiens

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<222> (1)..(137)

<223>

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<222> (138)..(1608)

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 ccctcccgcg gaggcctata aggggtgcggg ggggacgggg ccaggaggg gagtggagcc 120  
 tcaccagcca cgtcctc atg gcc ctg ctg ctc ttg ctg ttc ctg ggc ctc 170  
                   Met Ala Leu Leu Leu Leu Phe Leu Gly Leu  
                   1                  5                  10  
 ctg ggg ctc tgg ggg ctg ctc tgc gcc tgc gcc caa gac ccc tcc cca 218  
 Leu Gly Leu Trp Gly Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro  
                   15                  20                  25  
 gct gcc cgg tgg ccc ccg ggg cct cgc ccg ctg ccg ctc gtc ggg aac 266  
 Ala Ala Arg Trp Pro Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn  
                   30                  35                  40  
 ctg cac ttg ctg cgt ctg tgc caa cag gac cgg tcc ctg atg gag ctc 314  
 Leu His Leu Leu Arg Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu  
                   45                  50                  55  
 tca gaa cgc tac ggg ccg gtg ttc acc gtg cac ctg ggg cgc cag aag 362  
 Ser Glu Arg Tyr Gly Pro Val Phe Thr Val His Leu Gly Arg Gln Lys  
 60                  65                  70                  75  
 acg gtg gtg ctg acg ggg ttc gag gcg gtc aaa gag gcg ctg gcg ggc 410  
 Thr Val Val Leu Thr Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly  
                   80                  85                  90  
 ccc ggg cag gag ctg gcc gac cgg cct ccc atc gcc atc ttc cag ctc 458  
                                   Sida 6

## sequence\_listing.ST25.txt

Pro	Gly	Gln	Glu	Leu	Ala	Asp	Arg	Pro	Pro	Ile	Ala	Ile	Phe	Gln	Leu		
			95					100					105				
atc	cag	cga	ggt	gga	ggc	atc	ttc	ttc	tca	tct	ggg	gcg	cgc	tgg	agg		506
Ile	Gln	Arg	Gly	Gly	Gly	Ile	Phe	Phe	Ser	Ser	Gly	Ala	Arg	Trp	Arg		
		110					115				120						
gct	gcc	cgc	cag	ttc	acg	gtg	cgt	gcc	ctg	cac	agc	ctg	ggc	gtg	ggc		554
Ala	Ala	Arg	Gln	Phe	Thr	Val	Arg	Ala	Leu	His	Ser	Leu	Gly	Val	Gly		
		125				130					135						
cgg	gag	ccg	gtg	gct	gac	aag	att	ctg	cag	gag	ctg	aaa	tgc	ctc	tct		602
Arg	Glu	Pro	Val	Ala	Asp	Lys	Ile	Leu	Gln	Glu	Leu	Lys	Cys	Leu	Ser		
140					145					150					155		
ggg	cag	ctg	gat	ggc	tac	aga	ggc	cgg	ccc	ttc	ccg	ctg	gcc	cta	ctg		650
Gly	Gln	Leu	Asp	Gly	Tyr	Arg	Gly	Arg	Pro	Phe	Pro	Leu	Ala	Leu	Leu		
				160					165					170			
ggc	tgg	gct	ccc	tcc	aat	atc	acc	ttc	gcg	ctc	ctc	ttc	ggc	cgc	cga		698
Gly	Trp	Ala	Pro	Ser	Asn	Ile	Thr	Phe	Ala	Leu	Leu	Phe	Gly	Arg	Arg		
			175					180					185				
ttt	gac	tac	cgg	gac	ccc	gtg	ttt	gtg	tcc	ctg	ctg	ggt	ctc	atc	gat		746
Phe	Asp	Tyr	Arg	Asp	Pro	Val	Phe	Val	Ser	Leu	Leu	Gly	Leu	Ile	Asp		
		190					195					200					
gag	gtc	atg	gtc	ctc	ttg	ggg	tcc	cct	ggc	ctg	cag	ctg	ttc	aac	gtc		794
Glu	Val	Met	Val	Leu	Leu	Gly	Ser	Pro	Gly	Leu	Gln	Leu	Phe	Asn	Val		
	205					210					215						
tac	cca	tgg	ctc	ggg	gcc	ctg	ctc	cag	ctg	cac	cgg	ccc	gtc	ctg	cgc		842
Tyr	Pro	Trp	Leu	Gly	Ala	Leu	Leu	Gln	Leu	His	Arg	Pro	Val	Leu	Arg		
220					225					230					235		
aag	atc	gag	gag	gtc	cgt	gcc	att	ctg	agg	acc	ctc	ctg	gag	gcg	cgg		890
Lys	Ile	Glu	Glu	Val	Arg	Ala	Ile	Leu	Arg	Thr	Leu	Leu	Glu	Ala	Arg		
				240					245					250			
agg	ccc	cac	gtg	tgc	ccg	ggg	gac	ccc	gtg	tgc	agc	tat	gtg	gac	gcc		938
Arg	Pro	His	Val	Cys	Pro	Gly	Asp	Pro	Val	Cys	Ser	Tyr	Val	Asp	Ala		
			255					260					265				
ctg	atc	cag	cag	gga	cag	ggg	gat	gac	ccc	gag	ggc	ctg	ttt	gct	gag		986
Leu	Ile	Gln	Gln	Gly	Gln	Gly	Asp	Asp	Pro	Glu	Gly	Leu	Phe	Ala	Glu		
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gcc	aac	gcg	gtg	gcc	tgc	acc	ctg	gac	atg	gtc	atg	gcc	ggg	acg	gag		1034
Ala	Asn	Ala	Val	Ala	Cys	Thr	Leu	Asp	Met	Val	Met	Ala	Gly	Thr	Glu		
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acg	acc	tcg	gcc	acg	ctg	cag	tgg	gcc	gca	ctt	ctg	atg	ggc	cgg	cac		1082
Thr	Thr	Ser	Ala	Thr	Leu	Gln	Trp	Ala	Ala	Leu	Leu	Met	Gly	Arg	His		
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ccg	gac	gtg	cag	ggc	cgg	gtg	cag	gag	gag	cta	gac	cgc	gtg	ctg	ggc		1130
Pro	Asp	Val	Gln	Gly	Arg	Val	Gln	Glu	Glu	Leu	Asp	Arg	Val	Leu	Gly		
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cct	ggg	cgg	act	ccc	cgg	ctg	gag	gac	cag	cag	gct	ctg	ccc	tac	aca		1178
Pro	Gly	Arg	Thr	Pro	Arg	Leu	Glu	Asp	Gln	Gln	Ala	Leu	Pro	Tyr	Thr		
			335					340					345				
agc	gcc	gtg	ctc	cac	gag	gtg	cag	cgg	ttc	atc	acg	ctc	ctg	ccg	cac		1226
Ser	Ala	Val	Leu	His	Glu	Val	Gln	Arg	Phe	Ile	Thr	Leu	Leu	Pro	His		
		350					355					360					
gtg	ccc	cgc	tgc	acc	gcg	gcc	gac	aca	cag	ctg	ggc	ggc	ttc	ctg	ctc		1274

sequence\_listing.ST25.txt

Val	Pro	Arg	Cys	Thr	Ala	Ala	Asp	Thr	Gln	Leu	Gly	Gly	Phe	Leu	Leu	
365						370					375					
ccc	aag	ggc	acg	ccc	gtg	att	ccc	ctg	ctg	acc	tcg	gtg	ctc	ctg	gat	1322
Pro	Lys	Gly	Thr	Pro	Val	Ile	Pro	Leu	Leu	Thr	Ser	Val	Leu	Leu	Asp	
380					385					390					395	
gag	aca	cag	tgg	cag	acc	cca	ggc	cag	ttc	aac	ccc	ggc	cat	ttc	ctg	1370
Glu	Thr	Gln	Trp	Gln	Thr	Pro	Gly	Gln	Phe	Asn	Pro	Gly	His	Phe	Leu	
				400					405					410		
gac	gcg	aat	ggg	cac	ttt	gtg	aag	cgg	gag	gcc	ttc	ctg	cct	ttc	tct	1418
Asp	Ala	Asn	Gly	His	Phe	Val	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Phe	Ser	
			415					420					425			
gca	ggc	cgc	cgc	gtc	tgt	gtt	ggg	gag	cgc	ctg	gcc	agg	acc	gag	ctc	1466
Ala	Gly	Arg	Arg	Val	Cys	Val	Gly	Glu	Arg	Leu	Ala	Arg	Thr	Glu	Leu	
		430					435					440				
ttc	ctg	ctg	ttt	gcc	ggc	ctc	ctg	cag	agg	tac	cgc	ctg	ctg	ccc	ccg	1514
Phe	Leu	Leu	Phe	Ala	Gly	Leu	Leu	Gln	Arg	Tyr	Arg	Leu	Leu	Pro	Pro	
	445					450					455					
cct	ggc	gtc	agt	ccg	gcc	tcc	ctg	gac	acc	acg	ccc	gcc	cgg	gct	ttt	1562
Pro	Gly	Val	Ser	Pro	Ala	Ser	Leu	Asp	Thr	Thr	Pro	Ala	Arg	Ala	Phe	
460					465					470					475	
acc	atg	agg	ccg	agg	gcc	cag	gcc	ctg	tgt	gcg	gtg	ccc	agg	ccc	t	1608
Thr	Met	Arg	Pro	Arg	Ala	Gln	Ala	Leu	Cys	Ala	Val	Pro	Arg	Pro		
				480					485					490		
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accctctctc	ctcccacccc	acagctcgga	ctgctctggg	agggccctga	ggactccccc											1728
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ggcaaaaatg	gaaacactga	cccgggtgcgg	tggctcatgc	ctgtaatccc	agcacttttg											2328
gaggccgagg	caggcgaatc	acgaggtcag	gagttcgaga	ccagcctgcc	caacatggtg											2388
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<210> 10

<211> 137

<212> DNA

<213> Homo sapiens



## sequence\_listing.ST25.txt

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&lt;221&gt; promoter

&lt;222&gt; (1)..(137)

&lt;223&gt; -137 to -1 5'UTR of CYP2W1 gene

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ccctcccgcg gaggcctata aggggtgcggg ggggacgggg cccaggaggg gagtggagcc 120

tcaccagcca cgtcctc 137